

Exhibit 3: Key Variables in Assessing Laboratory Workload

Variable	Description
Number of victims	Generally, this is a straightforward estimate in the case of airline disasters that do not involve populated areas because the laboratory has access to the passenger manifest (although babies may not be included on the manifest). This estimate is more difficult for incidents that take place in office buildings, stadiums, etc. because the number and identity of victims are not known until long after the incident occurs.
Number of recoverable fragments	<p>It is important to distinguish between the degree of fragmentation and the number of recoverable fragments. In the World Trade Center incident, there was an incredible degree of fragmentation, with an average of only seven recovered fragments for each victim.</p> <p>Based on historical data, there are approximately five to eight fragments recovered per victim in airline disasters. Therefore, for general planning purposes, 10 would be a good estimate to use.</p>
Percentage of samples to be reworked	Some percentage of samples will need to be reanalyzed before they yield usable DNA profiles; 20 percent is a conservative estimate.
Number of personal items per victim	An estimate of the number of personal items will be provided for each victim. Historically, this is between five and eight. Note that usually not all of the items collected are analyzed; there should be a process to identify those items most likely to yield useful results.
Percentage of personal items to be reworked	Some percentage of personal items will not yield usable DNA profiles. Historically, 20 percent is a good estimate. When this occurs, the items are either reanalyzed or one of the other personal items is analyzed.
Personal items quality control samples	The laboratory should be prepared to reanalyze some percentage of all personal items samples as a quality control mechanism; 5 percent is common practice.
Number of kinship samples	Historically, three or four relatives per victim is a reliable estimate of the number of kinship samples. Note that buccal swabs nearly always produce complete DNA profiles, so it is not necessary to estimate rework.